
MAESRAH (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPArch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Sep 8 13:40:50 1999; MasPar time 75.04 Seconds
Tabular output not generated. 916,624 Million cell updates/sec

Title: >US-09-133-119-2
Description: (1-321) from US09133119.seq
Perfect Score: 321
N.A. Sequence: 1 GACATCTTGCTGACTCAGTC.....GGACAAATTTGGAGTAAAA 321
Comp: CTCGTAGACGACTGAGTCAG.....CCTGTTTAAACCTTCATTTT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 271905 seqs, 107135622 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40 41:part41 42:part42 43:part43
44:part44 45:part45 46:part46 47:part47 48:part48
49:part49 50:part50 51:part51 52:part52 53:part53
54:part54 55:part55 56:part56 57:part57 58:part58
59:part59 60:part60

Statistics: Mean 8.015; Variance 4.693; scale 1.708

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	321	100.0	321	37	V03615	9.02e-208
2	321	100.0	321	35	T07441	9.02e-208
3	291	90.7	1395	1	N50300	4.65e-186
4	286	89.1	381	40	V12262	1.91e-182
5	283	88.2	321	44	V26766	2.81e-180
6	279	86.9	321	7	Q32343	2.17e-177
7	277	86.3	720	44	V26770	6.04e-176
8	275	85.7	322	10	Q44714	1.68e-174
9	275	85.7	717	7	Q40463	1.68e-174

10	274	85.4	318	8	Q48766	Monoclonal antibody B	8.84e-174
11	274	85.4	429	30	T70811	Mouse anti-idiotypic	8.84e-174
12	273	85.0	381	32	T49338	CDNA encoding kappa l	4.66e-173
13	273	85.0	416	32	T49342	CDNA encoding kappa l	4.66e-173
14	273	85.0	416	32	T49344	CDNA encoding kappa l	4.66e-173
15	272	84.7	300	3	Q20306	B cell hybridoma l:5	2.45e-172
16	270	84.1	318	48	V54788	DNA encoding the light	6.80e-171
17	270	84.1	720	48	V34790	scfv comprising heavy	6.80e-171
18	269	83.8	322	6	Q36615	Anti-IL2R-beta antio	3.58e-170
19	267	83.2	486	7	Q43384	L-chain V-region of m	9.92e-169
20	265	82.6	794	24	T42033	Plasmid pMW152-225 fr	2.75e-167
21	265	82.6	2070	24	T42035	Plasmid pSW202-225 fr	2.75e-167
22	265	82.6	2793	24	T42039	Plasmid pMS238-5-225	2.75e-167
23	265	82.6	2793	24	T42040	Plasmid pMS238-225-5	2.75e-167
24	265	82.6	3177	24	T42041	Plasmid pMS240-5-225	2.75e-167
25	253	78.8	720	7	Q40462	Fv(TU27)	1.22e-158
26	219	68.2	416	32	T49345	CDNA encoding kappa l	3.24e-134
27	211	65.7	324	58	V71798	Marine vitronectin al	1.74e-128
28	201	62.6	486	7	Q43245	hIL2R Ab L chain v re	2.46e-121
29	197	61.4	381	11	Q64167	Sequence of mouse V-k	1.77e-118
30	193	60.1	5238	1	Q04654	Plasmid pBT111 encodi	1.26e-115
31	185	57.6	324	23	T33446	EGF receptor chimeric	6.36e-110
32	182	56.7	321	48	V49823	LM609 antibody light	8.69e-108
33	181	56.4	321	58	V71800	Humanised anti-alpha-	4.47e-107
34	181	56.4	338	58	V71802	Vitronectin alpha-v b	4.47e-107
35	179	55.8	363	29	T38510	Light chain coding se	1.18e-105
36	162	50.5	321	48	V49821	Vitaxin antibody ligh	1.36e-93
37	161	50.2	315	58	V71803	Jk gene segment	6.96e-93
38	161	50.2	315	58	V71805	Humanised anti-alpha-	6.96e-93
39	160	49.8	321	48	V49843	LM609 antibody light	3.55e-92
40	133	41.4	924	10	Q71872	Sequence coding human	3.65e-73
41	122	38.0	1204	2	Q11879	IgG light chain varia	1.77e-65
42	122	38.0	1242	2	Q11878	IB1 Igg aberrant ligh	1.77e-65
43	120	37.4	812	28	T37180	DNA fragment vk65.3,	4.38e-64
44	120	37.4	812	12	Q78852	Human v-kappa gene vk	4.38e-64
45	120	37.4	812	50	V38182	Human DNA fragment vk	4.38e-64

ALIGNMENTS

RESULT 1
ID V03615 standard; cDNA; 321 BP.
AC V03615;
DT 02-APR-1998 (first entry)
DE Coding sequence for light chain variable region used in chimeric Ab.
KW Tumour necrosis factor; human; hTNF; rheumatoid arthritis; malignancy;
KW anti-TNF chimeric antibody; inhibitor; therapy; diagnosis; infection;
KW chronic inflammatory disease; autoimmune disease; light chain;
KW neurodegenerative disease; variable region; ss.
OS Mus sp.
PN US5698195-A.
PD 16-DEC-1997.
PF 18-OCT-1994; 324799.
PR 18-OCT-1994; US-324799.
PR 18-MAR-1991; US-670827.
PR 18-MAR-1992; US-853606.
PR 11-SEP-1992; US-943852.
PR 29-JAN-1993; US-010406.
PR 02-FEB-1995; US-013413.
PR 04-FEB-1994; US-192061.
PR 04-FEB-1994; US-192093.
PR 04-FEB-1994; US-192102.
PR (GEN2) CENTOCOR INC.
PA (UNY-) UNIV NEW YORK MEDICAL CENT.
PI Daddona P, Ghayeb J, Knight D, Le J, Siegel S,
PI Vilcek J;
DR WPI: 98-051431/05.
DR P-ESDB; W40820.
PT Treatment of rheumatoid arthritis - with chimeric antibody directed
PT against tumour necrosis factor
PS Claim 15; Column 99-100; 93pp; English.
CC This sequence represents the coding sequence for the variable light chain
of a mouse antibody. This sequence can be used as part of the chimeric

CC antibody used in the method of the invention. The method of the invention
 CC is for treating rheumatoid arthritis in a human, and comprises
 CC administering to the human an effective tumour necrosis factor- (TNF)
 CC inhibiting amount of an anti-TNF chimeric antibody (Ab), where the
 CC anti-TNF chimeric Ab comprises a non-human variable region or a TNF
 CC antigen binding portion of the variable region, and a human constant
 CC region. The method can be used for in vitro, in situ and/or in vivo
 CC diagnosis and/or treatment of animal cells, tissues or pathologies
 CC associated with the presence of TNF. The Abs used in the method can also
 CC be used for removing TNF from a solution or cells, inhibiting one or more
 CC biological activities of TNF in vitro, in situ or in vitro. Such removal
 CC can include treatment methods of the invention for alleviating symptoms
 CC of pathologies involving TNF, such as bacterial, viral or parasitic
 CC infections, chronic inflammatory diseases, autoimmune diseases,
 CC malignancies and/or neurodegenerative diseases.

SQ Sequence 321 BP; 83 A; 72 C; 77 G; 89 T;

Query Match 100.0%; Score 321; DB 37; Length 321;

Best Local Similarity 100.0%; Pred. No. 9.02e-208;

Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 gacatcttgctgactcagtcctccagccatcctgtgtgagtcgccaggagaaagagtcagt 60

QY 1 GACATCTTGCTGACTCAGTCCTCCAGCCATCCTGTGTGAGTCCAGGAGAAAGAGTCAGT 60

Db 61 ttctctgcagggccagtcagtcctccagccatcctgtgtgagtcgccaggagaaagagtcagt 120

QY 61 TTCTCTGCAGGGCCAGTCAGTCCTCCAGCCATCCTGTGTGAGTCCAGGAGAAAGAGTCAGT 120

Db 121 aatggcttccaaaggtctctataaagatgcttctgtgagtcgccaggagaaagagtcagt 180

QY 121 AATGGTCTCCAAAGGCTCTCTATAAAGATGCTTCTGTGAGTCCAGGAGAAAGAGTCAGT 180

Db 181 aggtttagtcagtcagtcctccaaagatgcttctgtgagtcgccaggagaaagagtcagt 240

QY 181 AGGTTTAGTCAGTCAGTCCTCCAAAGATGCTTCTGTGAGTCCAGGAGAAAGAGTCAGT 240

Db 241 gaagatatgcagattattactgtcaacaaagtcagtcagtcgccaggagaaagagtcagt 300

QY 241 GAAGATATGTCAGATTATTACTGTCAACAAAGTCAGTCAGTCGCCAGGAGAAAGAGTCAGT 300

Db 301 gggacaaatttggagtaaaaa 321

QY 301 GGGACAAATTTGGAAGTAAAA 321

RESULT 2

ID T87441 standard; cDNA; 321 BP.

AC T87441;

DT 12-JAN-1998 (first entry)

DE Humanised cA2 light chain variable region.

KW TNF: tumour necrosis factor; Crohn's disease; cA2 antibody; ss.

OS Synthetic.

PN US5656272-A.

PF 12-AUG-1997.

PI 18-MAR-1991; 670827.

PR 04-FEB-1994; US-192102.

PR 18-MAR-1991; US-670827.

PR 18-MAR-1992; US-853606.

PR 11-SEP-1992; US-943852.

PR 26-JAN-1993; US-010406.

PR 02-FEB-1993; US-013413.

PA (CENZ) CENTOCOR INC.

PA (UINY-) UNIV NEW YORK MEDICAL CENT.

PI Dadoona P, Ghayeb J, Knight D, Le J, Siegel SA;

PI Vilcek J;

DR WPI; 97-414547/38.

DR P-PSDB: W28531.

PT Treatment of Crohn's disease - by administering humanised cA2

PS antibody specific for tumour necrosis factor

PS Disclosure; Fig 16A; 87pp; English.

CC An anti-TNF chimeric antibody may be administered for treating

CC TNF-alpha mediated Crohn's disease in a human.

CC The anti-TNF chimeric antibody competitively inhibits binding of
 CC TNF to monoclonal antibody cA2. The anti-TNF antibody does
 CC not bind to one or more epitopes in amino acids 11-13, 37-42,
 CC 49-57 or 155-157 of hTNF, but does bind to one or more epitopes
 CC included in amino acids between 87-108 or both 87-108 and 59-80
 CC of hTNF.

SQ Sequence 321 BP; 83 A; 72 C; 77 G; 89 T;

Query Match 100.0%; Score 321; DB 35; Length 321;

Best Local Similarity 100.0%; Pred. No. 9.02e-208;

Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 gacatcttgctgactcagtcctccagccatcctgtgtgagtcgccaggagaaagagtcagt 60

QY 1 GACATCTTGCTGACTCAGTCCTCCAGCCATCCTGTGTGAGTCCAGGAGAAAGAGTCAGT 60

Db 61 ttctctgcagggccagtcagtcctccagccatcctgtgtgagtcgccaggagaaagagtcagt 120

QY 61 TTCTCTGCAGGGCCAGTCAGTCCTCCAGCCATCCTGTGTGAGTCCAGGAGAAAGAGTCAGT 120

Db 121 aatggcttccaaaggtctctataaagatgcttctgtgagtcgccaggagaaagagtcagt 180

QY 121 AATGGTCTCCAAAGGCTCTCTATAAAGATGCTTCTGTGAGTCCAGGAGAAAGAGTCAGT 180

Db 181 aggtttagtcagtcagtcctccaaagatgcttctgtgagtcgccaggagaaagagtcagt 240

QY 181 AGGTTTAGTCAGTCAGTCCTCCAAAGATGCTTCTGTGAGTCCAGGAGAAAGAGTCAGT 240

Db 241 gaagatatgcagattattactgtcaacaaagtcagtcagtcgccaggagaaagagtcagt 300

QY 241 GAAGATATGTCAGATTATTACTGTCAACAAAGTCAGTCAGTCGCCAGGAGAAAGAGTCAGT 300

Db 301 gggacaaatttggagtaaaaa 321

QY 301 GGGACAAATTTGGAAGTAAAA 321

RESULT 3

ID N90300 standard; DNA; 1395 BP.

AC N90300;

DT 1-NOV-1989 (first entry)

DE Insert coding for light chain murine variable region

KW Recombinant DNA; chimeric monoclonal antibody; light chain; heavy chain;

KW variable region; human carcinoembryonic antigen; cell line CE25.

PH Key Location/Qualifiers

FT cds 733..1320

FT /*tag= a

FT /*tag= b

FT intron 781..987

PN EP-323806-A.

PD 12-JUL-1989.

PF 28-DEC-1988; 810898.

PR 05-JAN-1988; GB-00077.

PA (CIBA) Ciba-Geigy AG.

PI Hardman N, Gill LL, de Winter RFJ, Wagner K, Heusser C;

DR WPI; 89-200701/28.

DR P-PSDB: P90479.

PT Chimeric monoclonal antibody to human carcinoembryonic antigen

PT - consisting of variable regions of mouse origin and human constant

PT regions, for cancer diagnosis and therapy.

PS Claim 25; page 35; 53pp; English.

CC The recombinant DNA is an insert coding for a light chain murine

CC variable region, which is specific for human carcinoembryonic antigen and

CC originates from genomic DNA of the cell line CE 25. See also P90479.

SQ Sequence 1395 BP; 397 A; 240 C; 276 G; 482 T;

Query Match 90.7%; Score 291; DB 1; Length 1395;

Best Local Similarity 95.3%; Pred. No. 4.65e-186;

Matches 306; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 1000 gacatcttgctgactcagtcctccagccatcctgtgtgagtcgccaggagaaagagtcagt 1059

QY 1 GACATCTTGCTGACTCAGTCCTCCAGCCATCCTGTGTGAGTCCAGGAGAAAGAGTCAGT 60

QY	1	GACATCTTGCTGACTCAGTCTCCAGCCATCCCTGCTGTGAGTCCAGGAAAGAGTCAGT	60
Db	61	ttctctctcagggccagtcagagaattggcacaagcatatactctggtatcagcaaaagaaca	120
QY	61	TTCTCTCGCAGGGCCAGTCAGTTCGTTGCTCAAGCATCCACTGGTATCAGCAAAAGACA	120
Db	121	aatgggtctccagggtctctcataaagtatgctctctgagtcctatctctctgggatacccttcc	180
QY	121	AATGGGTCTTCCAAAGGTTCTCATAAAGATATGCTTCTGAGTCTATGCTGGGATCCCTTCC	180
Db	181	agattttagtggcagtgatcaggacagagattttactcttaaacatacaacagttggagttct	240
QY	181	AGGTTTAGTGGCAGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT	240
Db	241	gaagatattgcagtttattactgtcacaacagataatagctggccattccagcttcgggtctcg	300
QY	241	GANGATATTGCAGATTATTACTGTCAACAAGTCATAGCTGGCCATTACGTTCCGGCTCG	300
Db	301	gggacaaaagtggaaaataaaa	321
QY	301	GGGACAAATTTGGAAGTAAAA	321

RESULT	6	
ID	Q43243 standard; DNA; 321 BP.	
AC	Q43243;	
DE	13-OCT-1993 (first entry)	
DT	B-B10 MAb L chain V region DNA.	
DE	Complementarity-determining region; CDR; humanised; antibody; hIL2R;	
KW	human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;	
KW	monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;	
KW	region; PCR; framework; plasmid; heavy; H; light; L; ss.	
QS	Mus musculus.	
PN	WO9311238-A.	
PN	10-JUN-1993.	
PF	03-DEC-1992; J01583.	
PR	06-DEC-1991; JP-323319.	
PA	(BIOT) BIOTEST PHARMA GMBH.	
PA	(INNO-) INNOTHERAPIE LAB.	
PA	(SUMU) SUMITOMO PHARM CO LTD.	
PI	Gomi H, Nakatani T, Noguchi H, Wijdenes J;	
DR	WPI: 93-197057/24.	
DR	P-PSDB; R37610.	
PT	Humanised antibody comprising - CDR region of mouse MAB B-B10	
PT	specific for IL-2 receptor useful for treating carcinoma	
PT	expressing IL-2 receptor	
PS	Disclosure: Fig 2: 62pp: English.	
CC	The sequences given in Q43242-43 encode the heavy (H) and light (L)	
CC	chain variable (V) regions of the murine anti-human IL-2 receptor	
CC	monoclonal antibody (MAB) B-B10, respectively. This MAB was used in	
CC	the construction of a humanised antibody (AB) which binds specifically	
CC	to human interleukin (IL)-2 receptor (hIL2R). The complementarity-	
CC	determining regions (CDRs) for the hIL2R MAB were derived from B-B10	
CC	(see also R37599-04). The hIL2R MAB is antagonistic to the binding	
CC	of IL-2 to the IL-2 receptor on human T-cells. It also inhibits	
CC	the human mixed lymphocyte reaction. The cDNA encoding the variable	
CC	(V) region of the B-B10 Ab was cloned by PCR and sequenced (see also	
CC	Q43226-32 and Q43233-36). A human Ab with high levels of amino acid	
CC	sequence homology to the murine sequence was selected and the	
CC	framework of this Ab was bound with the B-B10 V region CDR and a	
CC	part of the framework to design several kinds of the humanised B-B10	
CC	V region. The DNA sequence coding this humanised B-B10 was	
CC	synthesised and a plasmid expressing humanised B-B10 was constructed.	
SQ	Sequence 321 BP; 82 A; 74 C; 81 G; 84 T;	

Db	61	ttctctctgcaggccagtcagaccattggcacaagcatcacctggttatcagcggaagaa	120
Qy	61	TTCTCTCGCAGGCCAGTCAGTTGGCTCAAGCATCCACTGGTATTACGACAAAGACA	120
Db	121	aatggttctccaaggcttctcataaagtagctctctgagtcctatctctgggacccctcc	180
Qy	121	AATGGTTCTCCAAGGCTTCTCAATAAGTAGCTCTGAGTCTATGCTGGGATCCCTTCC	180
Db	181	aggtttagtgccagtgagtcaggagcagattttactccttagcatcaaacagtgtagtct	240
Qy	181	AGGTTTAGTGGCAGTGGATCGGCACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT	240
Db	241	gaagatattgcagatattactctgcacaaagtagtgctggccgctcacgtcttcgggtgc	300
Qy	241	GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCTGGCCATTACGTTCCGCTCG	300
Db	301	gggaccaagctggagctgaaa	321
Qy	301	GGGACAAATTTGGGAAGTAAAA	321

RESULT	7	
ID	V26770 standard; cDNA; 720 BP.	
AC	V26770;	
DE	14-SEP-1998 (first entry)	
DT	Anti-gp54 Mab 48-127 scFv cDNA.	
DE	Single chain antibody; scFv; monoclonal antibody; MAB; 48-127;	
KW	trop-2; gp54; antigen; cancer marker; bladder cancer;	
KW	breast cancer; cervix cancer; prostate cancer; metastasis;	
KW	diagnosis; therapy; immunotherapy; ds.	
OS	Chimeric - Mus sp.	
OS	Chimeric - Synthetic.	
FH	Key Location/Qualifiers	
FT	CDS 3..720	
FT	/*tag= a	
PN	WO9812227-A1.	
PD	26-MAR-1998.	
PF	19-SEP-1997; CA0690.	
PR	19-SEP-1996; US-026320.	
PA	(DIAG-) DIAGNOCURE INC.	
PI	Darveau A, Fradet Y;	
DR	WPI; 98-212711/19.	
DR	P-PSDB; W26799.	
PT	New recombinant antibodies to gp54 antigen - used for the detection	
PT	of cancers and metastases and for therapy of cancers expressing the	
PT	gp54 antigen	
PS	Claim 11; Fig 7; 33pp: English.	
CC	This cDNA sequence codes for a novel single chain antibody	
CC	(scFv, see W26799) that comprises the heavy chain variable region	
CC	(see W26796) of murine monoclonal antibody 48-127 linked to the	
CC	light chain variable region (see W26795) of 48-127 via a peptide	
CC	linker. It is obtained by PCR amplification of 48-127 light chain	
CC	and heavy chain cDNAs (see also V26766-67), and PCR-mediated	
CC	ligation of amplified fragments. The construct has been cloned	
CC	into vector pFUS-CMV, and the scfv expressed in transfect COS-7	
CC	cells. The scfv recognises an epitope of gp54 antigen (trop-2), a	
CC	cancer marker expressed at the surface of bladder, breast, uterine	
CC	and prostate cancers. It can be used to detect cancers and	
CC	micrometastases, e.g. bladder, prostate, breast or uterine cervix	
CC	cancers, and may be linked to specific toxins for use in cancer	
CC	therapy. Such scfvs are not immunogenic and are distributed and	
CC	captured by gp45-bearing target cells more quickly than conventional	
CC	antibodies.	
SQ	Sequence 720 BP; 178 A; 160 C; 200 G; 182T;	

Query Match	86.3%	Score 277;	DB 44;	Length 720;
Best Local Similarity	93.4%;	Pred. No. 6,04e-176;		
Matches	298;	Mismatches 0;	Indels 0;	Gaps
Db	402	gacgttatgatgacgcgaactctccagccatctctgtgagtcacgaggaagagtcagt	461	
QY	1	GACATCTTGCTGACTCAGTCTCCAGCCATCTCTGTGAGTCCAGCAAGAGTCACT	60	

REFERENCE	Mus.
AUTHORS	1 (bases 1 to 354) Fiorentini,S., Matczak,E., Reitz,M.S. Jr., Gallo,R.C., Keydar,I. and Watkins,B.A.
TITLE	Humanization of an antibody recognizing a breast cancer specific epitope
JOURNAL	Immunotechnology (1996) In press
REFERENCE	2 (bases 1 to 354)
AUTHORS	Fiorentini,S., Matczak,E., Reitz,M.S. Jr., Gallo,R.C., Keydar,I. and Watkins,B.A.
TITLE	Direct Submission
JOURNAL	Submitted (07-OCT-1996) Lab. of Tumor Cell Biology, National Cancer Institute, 37 Convent Drive, Room 6A11, Bethesda, MD 20892-4255, USA
FEATURES	Location/Qualifiers
Source	1..354 /organism="Mus musculus" /strain="BALB/c" /db_xref="taxon:10090" /tissue_type="hybridoma" /rearranged
V_region	1..354 /gene="IgGVH"
gene	1..354 /gene="IgGVH" <1..>354 /gene="IgGVH"
CDS	/note="recognizes breast cancer associated antigen Muc-1" /codon_start=1 /product="immunoglobulin H23 rearranged heavy chain variable region" /protein_id="AAB38290.1" /db_xref="PID:g1710423" /db_xref="GI:1710423" /translation="LEVKLVESGGVLVOPGRMKLSCVSGFTFSNYMMNVVROSPER GLEWAEIRLKSNNATYHAEYSVKGRFTISRDDSSVYLQNNLRADETGIYCTVS IGFAYWGGTGLGTSS"
BASE COUNT	91 a 69 c 98 g 96 t
ORIGIN	
Query Match	72.8%; Score 260; DB 32; Length 354;
Best Local Similarity	94.2%; Pred. No. 3.29e-193;
Matches	277; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Db	4 GAGGTGAAGCTGTGTGAGTCTGAGGAGGCTTGGTCAACCTCGAGATCCATGAACCTC 63
QY	1 GAAGTGAAGCTTGAGGAGTCTGAGGAGGCTTGGTCAACCTCGAGATCCATGAACCTC 60
Db	64 TCCTGTGTGCCCTCTGGATCACTTTTCAGTAACCTACTGGATGAACCTGGGTCGCCAGTCT 123
QY	61 TCCTGTGTGCCCTCTGGATCACTTTTCAGTAACCTACTGGATGAACCTGGGTCGCCAGTCT 120
Db	124 CCAGAGAAGGGCTTGTGAGTGGGTGCTGAGATAGATTGAAATCTTAATAATTATGCAACA 183
QY	121 CCAGAGAAGGGCTTGTGAGTGGGTGCTGAAATTAGATCAAAATCTATTAACTTGTGCAACA 180
Db	184 CATTATCGCGAGTCTGTGAAGGGAGGTTCCACCATCTCAAGATGATATCCAAAGTAGT 243
QY	181 CATTATCGCGAGTCTGTGAAGGGAGGTTCCACCATCTCAAGATGATATCCAAAGTAGT 240
Db	244 GTCTACTGCAATGAACAACTTTAAGAGCTGAAGACACTGGCATTTTATTACTCT 297
QY	241 GTCTACTGCAATGACCGACCTTAAAGACTGAAGACACTGGCGTTTATTACTCT 294
RESULT	10
LOCUS	MUSIGHHT 427 bp mRNA ROD 22-MAY-1991
DEFINITION	Mouse Ig mu-chain (J606 family) mRNA V-region (VJ), from hybridoma BC-1004-mu.
ACCESSION	M17167 J02815
NID	g195413
VERSION	M17167.1 GI:195413
KEYWORDS	J-region; V-region; immunoglobulin heavy chain; immunoglobulin

mu-chain.
Mouse (BALB/c) anti-bloodgroup A hybridoma, cDNA to mRNA, clone BC-1004-mu.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 427)
AUTHORS Chen, H.-T., Kabat, E.A., Lundblad, A. and Ratcliffe, R.M.
TITLE Nucleotide and translated amino acid sequences of cDNA coding for the variable regions of the light and heavy chains of mouse hybridoma antibodies to blood group A and B substances
JOURNAL J. Biol. Chem. 262, 13579-13583 (1987)
MEDLINE 88007582
COMMENT Draft entry and printed copy of sequence for [1] kindly provided by E.A. Kabat, 04-AUG-1987.
FEATURES
source Location/Qualifiers
1..427
/organism="Mus musculus"
/db_xref="taxon:10090"
11..67
/note="Ig mu-chain"
11..>341
/note="Ig mu-chain precursor V-region (VJ)"
/codon_start=1
/protein_id="AAA38296.1"
/db_xref="PID:G553990"
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68..>427
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BASE COUNT 112 a 85 c 113 g 117 t
ORIGIN Chromosome 12.
Query Match 72.8%; Score 260; DB 32; Length 427;
Best Local Similarity 86.5%; Pred. No. 3.29e-193;
Matches 308; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
Db 68 GAAGTGAAGCTTGAGAGCTCTGGAGGAGGCTTGGTGCACCTGGAGATCCATGAACCTC 127
QY 1 GAAGTGAAGCTTGAGAGCTCTGGAGGAGGCTTGGTGCACCTGGAGATCCATGAACCTC 60
Db 128 TCTTGTGCTCTCGATTACCTTTTGTAGTACGCTGGATGACCTGGGTCGCCAGTCT 187
QY 61 TCTGTGTTGCTCTCGATTACCTTTTGTAGTACGCTGGATGACCTGGGTCGCCAGTCT 120
Db 188 CCAGAGAAGGGGCTTGAATGGTGTGCTGAACCTTAGAAGCAAGCTCATATCATGCAACA 247
QY 121 CCAGAGAAGGGGCTTGAATGGTGTGCTGAACCTTAGAAGCAAGCTCATATCATGCAACA 180
Db 248 TACTATCTAGTCTGTGAAGGAGGCTTCAACCTCTCAAGAGATGATTCACCAAGTAAAT 307
QY 181 CATTATCGGAGTCTGTGAAGGAGGCTTCAACCTCTCAAGAGATGATTCACCAAGTAAAT 240
Db 308 GTTCTACCTCAATGACACCTTAAAGCTTGAAGACACTGGCATTTATTACTTACACAGG 367
QY 241 GTCTACCTCAATGACACCTTAAAGCTTGAAGACACTGGCATTTATTACTTACACAGG 300
Db 368 GATTACTACGGTGGCGAGTTTGTCTTACTGGGCGCAAGGACTCTGGTCACTGCTC 423
QY 301 AATTACTACGGTAGTACCTACGACTACTGGGCGCAAGGACCACTCTCAGACTCTC 356
RESULT 11
LOCUS MUSIGHSA 305 bp mRNA ROD 04-AUG-1994
DEFINITION Mouse Ig active H-chain (GAC1) mRNA V-region, from hybridoma 66.3E3, partial cds.
ACCESSION M32051
NID g195976
VERSION M32051.1 GI:195976
KEYWORDS V-region; immunoglobulin heavy chain; processed gene.

ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 305)
AUTHORS Jarvis, C.D., Cannon, L.E. and Stavnezer, J.
TITLE Mouse antibody response to group A streptococcal carbohydrate
JOURNAL J. Immunol. 143, 4213-4220 (1989)
MEDLINE 90079033
FEATURES
source Location/Qualifiers
1..305
/organism="Mus musculus"
/db_xref="taxon:10090"
11..11
/note="Ig H-chain V-region intron"
12..>305
/note="Ig H-chain V-region, X"
BASE COUNT 85 a 55 c 85 g 80 t
ORIGIN Chromosome 12.
Query Match 72.0%; Score 257; DB 32; Length 305;
Best Local Similarity 93.9%; Pred. No. 1.33e-190;
Matches 275; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Db 13 GAAGTGAAGCTTGAGAGCTCTGGAGGAGGCTTGGTGCACCTGGAGATCCATGAACCTC 72
QY 1 GAAGTGAAGCTTGAGAGCTCTGGAGGAGGCTTGGTGCACCTGGAGATCCATGAACCTC 60
Db 73 TCTGTGTTGCCCTCTGGATTCACCTTTTCAGTAACTACTGGATGTGCTGGGTCGCCAGTCT 132
QY 61 TCTGTGTTGCCCTCTGGATTCACCTTTTCAGTAACTACTGGATGTGCTGGGTCGCCAGTCT 120
Db 133 CCAGAGAAGGGGCTTGGATGGGTTGCTGAATAGATGAATCTAATAATTATGCAACA 192
QY 121 CCAGAGAAGGGGCTTGGATGGGTTGCTGAATAGATGAATCTAATAATTATGCAACA 180
Db 193 CATTATCGGAGTCTGTGAAGGAGGCTTCCACCTCTCAAGAGATGATTCACCAAGTAAAT 252
QY 181 CATTATCGGAGTCTGTGAAGGAGGCTTCCACCTCTCAAGAGATGATTCACCAAGTAAAT 240
Db 253 GTTCTACCTCAATGACACCTTGAAGGCTTGAAGGCTGAAGACACTGGAAATTTATTACTG 305
QY 241 GTTCTACCTCAATGACACCTTGAAGGCTTGAAGGCTGAAGACACTGGGCTTTATTACTG 293
RESULT 12
LOCUS MUSIGHRV 306 bp mRNA ROD 15-JUN-1990
DEFINITION Mouse Ig active H-chain (GAC1) mRNA V-region, from hybridoma 80.1B5, partial cds.
ACCESSION M32046
NID g195971
VERSION M32046.1 GI:195971
KEYWORDS V-region; immunoglobulin heavy chain; processed gene.
SOURCE Mouse (strain 80.1B5), cDNA to mRNA, anti-GAC hybridoma 80.1B5.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 306)
AUTHORS Jarvis, C.D., Cannon, L.E. and Stavnezer, J.
TITLE Mouse antibody response to group A streptococcal carbohydrate
JOURNAL J. Immunol. 143, 4213-4220 (1989)
MEDLINE 90079033
FEATURES
source Location/Qualifiers
1..306
/organism="Mus musculus"
/db_xref="taxon:10090"
11..11
/note="Ig H-chain V-region intron"
12..>306
/note="Ig H-chain V-region, X"
BASE COUNT 85 a 56 c 85 g 80 t

Qy	181	CATTATCGGAGTCTGTGAAGGAGGAGTTCAACATCTCAAGAGATGATCCAAAGTCT	240
Db	253	GTCTACCTGCAAAATGAACAGCTTAAGGCGTGAAGACACTGGAATTTATTACTG	305
Qy	241	GTCTACCTGCAAAATGACCGACTTAAGAAGTGAAGACACTGGCGTTTATTACTG	293
RESULT	14		
LOCUS	MMU03110	366 bp	12-SEP-1994
DEFINITION	Mus musculus BALB/c anti-glycophorin A type M Ig heavy chain mRNA,	partial cds.	
ACCESSION	U03110		
NID	9414566		
VERSION	U03110.1	GI:414566	
KEYWORDS	house mouse.		
SOURCE	Mus musculus		
ORGANISM	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 366)		
AUTHORS	Spitalnik, S.L.		
TITLE	Restricted VH usage by murine hybridomas directed against the human N, but not M, antigen		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 366)		
AUTHORS	Spitalnik, S.L.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-NOV-1993) Steven L. Spitalnik, Department of Pathol. and Lab. Medicine, University of Pennsylvania, 36th & Hamilton walk, 220 John Morgan Building, Philadelphia, PA 19104, USA		
FEATURES	Location/Qualifiers		
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	/db_xref="taxon:10090"		
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	/cell_type="hybridoma"		
	<1..>366		
CDS	/standard_name="anti-glycophorin A type M, antibody 425"		
	/codon_start=1		
	/product="immunoglobulin heavy chain"		
	/protein_id="AAA21378.1"		
	/db_xref="PID:g414567"		
	/db_xref="GI:414567"		
	/translation="EVOLVESGGLVQPGSMKVCIASGFTTSHVMNVRSPKGLWVAEIRLKSNNYATHHAESVGRFTISRDDSKSVYLOMNLRAEDTGIIYCTRRL YGYHGYMDYWGQTSVTVIS"		
V.segment	<1..300		
D.segment	301..318		
J.segment	319..366		
BASE COUNT	100 a	99 g	92 t
ORIGIN			
Query Match	72.0%;	Score 257;	DB 32; Length 366;
Best Local Similarity	91.3%;	Pred. No. 1,33e-190;	
Matches	284;	Conservative 0;	Mismatches 27; Indels 0; Gaps 0;
Db	1	GAAGTCAGTTGGTGGAGCTCTGGAGGAGCGCTTGGTGCAACCTGGAGGATCCATGAAAGTC	60
Qy	1	GAAGTGAAGCTTGAGGAGCTCTGGAGGAGCGCTTGGTGCAACCTGGAGGATCCATGAAAGTC	60
Db	61	TCCTGTATTGCTCTGGATTTCACCTTCAGTCACACTGGATGAAGTCCGCGCAGTCT	120
Qy	61	TCCTGTGTGGCTCTGGATTTCATTTTCAGTAACCACTGGATGAAGTCCGCGCAGTCT	120
Db	121	CCAGAGAAGGGCGTTGAGTGGGTCGAGAAATTAGATTGAATCTAATAATTATGCAACA	180
Qy	121	CCAGAGAAGGGCGTTGAGTGGGTCGCTGAAATTAGATCAAAATCTAATAATTGCAACA	180
Db	181	CATCATCGGAGTCTGTGAAAGGAGGAGTTCCACCATCTCAAGAGATGATTCCAAAGTAGT	240
Qy	181	CATCATCGGAGTCTGTGAAAGGAGGAGTTCCACCATCTCAAGAGATGATTCCAAAGTAGT	240

QY 181 CATTATCGGAGTCTGTGAAGGGAGGTTACCATCTCAAGAGATGATTCCAAAGTGCT 240
Db 241 GTCCTACCTGCAAAAGAACACTTAAGACTGAAGACTGCGCATTATTACTGTACCAGG 300
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QY 241 GTCCTACCTGCAAAAGAACACTTAAGACTGAAGACTGCGCATTATTACTGTACCAGG 300
Db 301 CGGGGCTACGG 311
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QY 301 AATTACTACGG 311

RESULT 15
LOCUS MUSIGHRU 314 bp mRNA ROD 15-JUN-1990
DEFINITION Mouse Ig active H-chain (GAC1) mRNA V-region, from hybridoma
68.3D3, partial cds.
ACCESSION M32045
NID G195970
VERSION M32045.1 GI:195970
KEYWORDS V-region; immunoglobulin heavy chain; processed gene.
SOURCE Mouse (strain A/J), cDNA to mRNA, anti-GAC hybridoma 68.3D3.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 314)
AUTHORS Jarvis,C.D., Cannon,L.E. and Stavnezer,J.
TITLE Mouse antibody response to group A streptococcal carbohydrate
JOURNAL J. Immunol. 143, 4213-4220 (1989)
MEDLINE 90079033
FEATURES Location/Qualifiers
source 1..314
/organism="Mus musculus"
/db_xref="taxon:10090"
intron <1..11
/note="Ig H-chain V-region intron"
exon 12..>314
/note="Ig H-chain V-region, X"
BASE COUNT 88 a 58 c 85 g 82 t 1 others
ORIGIN Chromosome 12.

Query Match 71.7%; Score 256; DB 32; Length 314;
Best Local Similarity 93.8%; Pred. No. 9.80e-190;
Matches 274; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Db 14 AAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAACCTCT 73
QY 2 AAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAACCTCT 61
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Db 74 CCTGTGTGCTCTGGATTCACTTTCACTAAGTCTGCTGGATGCTGGTCCGCCAGTCTC 133
QY 62 CCTGTGTGCTCTGGATTCACTTTCACTAAGTCTGCTGGATGCTGGTCCGCCAGTCTC 121
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Db 134 CAGAGAGGGAGCTTGAAGGGTGGTGGTGAATAGATTGAATCTGATTAATTATGCAACAC 193
QY 122 CAGAGAGGGGCTTGAAGGGTGGTGGTGAATAGATTGAATCTGATTAATTATGCAACAC 181
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Db 194 ATTATGGGAGCTCTGTAAGGGAGGTTCCACCATCTCAAGAGATGATTCCTCAAAAGTCTG 253
QY 182 ATTATGGGAGCTCTGTAAGGGAGGTTCCACCATCTCAAGAGATGATTCCTCAAAAGTCTG 241
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Db 254 TCTACCTGCAAAAGAACACTTAAGGGCTGAAGACACTGGAATTTATTACTG 305
QY 242 TCTACCTGCAAAAGAACACTTAAGAACTGAAGACACTGGCGTTTATTACTG 293
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